REMARKS

Claims 1-3, 11, and 13-25 are pending in the present application. It appears that the Examiner has examined claims 1-3, 11, 13, 16-20 and 23-24. Claims 14-15, 21-22 and 25 appear to be withdrawn from consideration as being drawn to a non-elected invention. Claims 1 and 17 are independent claims.

Applicants have amended the specification to recite divisional status of this application. Applicants have not raised any issue of new matter.

Foreign Priority

The Examiner reports that foreign priority documents have not been received; however, this application is a Division of U.S. Application 08/676,882, July 3, 1996, now U.S. Patent 6,100,241. The priority documents are in the parent application, but we can easily file a copy of EP 95 201 801.8, filed July 3, 1995.

More importantly, this application should have at least a priority date of the parent application 08/676,882, filed July 3, 1996, because this application is a division of 08/676,882.

Drawings

Applicants will address the issues asserted on form PTO form 948 when the application has been indicated as being allowable.

Issue Under 35 U.S.C. §112

Claims 1-3, 11, 16-20, 23 and 24 stand rejected under 35 U.S.C. §112, first paragraph as allegedly having a specification that enables an isolated 37 kD protein from Eimeria acervulina with amino acid sequence set forth in SEQ ID NO: 2 and a vaccine comprising the 37 kD protein, but failing to provide a enabling disclosure for any fragment of the isolated protein.

Applicants traverse this rejection. First of all, Applicants have not claimed "any fragment of the isolated protein." Applicants have clearly claimed: An isolated protein comprising one or more immunoreactive and/or antigenic determinants of Eimeria lactate dehyrdogenase (LDH), wherein said isolated protein is found intracellularly in Eimeria. Only those fragment that are immunoreactive and/or antigenic determinants of Eimeria LDH are within the scope of the present invention.

The important terms to a skilled artisan relating to the protein parts that define the present invention are: "immunoreactive and/or antigenic determinants"; "a biologically active variant", and "an immunologically active part"

Immunoreactive and/or antigenic determinants of Eimeria lactate dehydrogenase are disclosed on page 6, lines 12 through 15. Detailed definitions are presented on page 8, line 27 through page 9, line 2 of the description. Routine techniques

for determining which fragments are immunogenic determinants are disclosed on page 9, lines 3 through 27. Both PEPSCAN and computer analyses allow the routine prediction of antigenic determinants. An illustration of the effectiveness of using these methods was published by H. Margalit et al. (1987, J. of Immunol., vol. 138, p. 2213-2229) who describe success rates of 75% in the prediction of epitopes using such methods.

Biologically functional equivalents or variants are described on page 7, lines 12 through 16 of the description. Commonly observed protein modifications are disclosed on page 7, lines 4 - 11. The equivalents and variants are defined on page 7, lines 17 through 25. As is specifically stated, such equivalent or variant proteins may be derived by insertions or deletion, but: ". . . retain one or more immunogenic determinants of the Eimeria antigens . . .".

A description of biological functional equivalents, for instance proteins carrying conserved amino acid mutations arising through evolutionary variations between Eimeria strains, is presented on page 7, line 26 through page 8, line 20. As is stated in lines 16-20 on page 8: "Such amino acid substitutions of the exemplary embodiments of this invention are within the scope of the invention as long as the resulting proteins **retain their immunoreactivity**" (emphasis added).

Methods to obtain such fragments are disclosed on page 8 line 27 through page 9, line 2.

An immunologically active part of the protein in SEQ ID NO: 2 can be determined and obtained in ways similar to the immunoreactive and/or antigenic determinants, see above.

Finally, Applicants submit that methods for establishing LDH activity of parts of the Eimeria protein of the invention have been well known in the art for many years. Detection of LDH enzyme activity is a standard technique in clinical chemistry labs in all major hospitals, for instance as a marker for myocardial or other diseases (reviewed by: P. Wolf, 1989, Clin. Lab. Med., vol. 9, p. 655-665).

Interestingly, measurement of LDH activity has also been described as a test for determining Plasmodium parasitemia (M. Makler and D. Hinrichs, 1993, Am. J. Trop. Med. Hyg., vol. 48, p. 205-210). *Abstracts are enclosed.*

"The test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation." In re Buchner, 929 F.2d 660, 661, 18 U.S.P.Q.2d 1331, 1332 (Fed. Cir. 1991). Also, the MPEP §2164.01 states that "[a] patent need not teach, and preferably omits, what is well known in the art." The determination of immunogenic and/or antigenic fragments of a protein is well known in the art and a skilled artisan would not suffer an undue burden of experimentation in obtaining the claimed scope of the present invention.

Issue Under 35 U.S.C. §102(e)

Claims 1-3, 11, 16-20 and 23-24 stand rejected under 35 U.S.C. §102(e) as being anticipated by Kok '241 (USP 6,100,241). Applicants traverse this rejection.

This rejection is completely improper. Kok '241 is the parent of this application, as Applicants noted in the Response of March 22, 2002 and now stated on the first line and of the first page of the present specification. Therefore, Kok '241 cannot be used as prior art against this application.

Applicants respectfully request withdrawal of the 35 U.S.C. §102 rejection.

Issue Under 35 U.S.C. §102(e)

Claims 1-3, 11, 16-20 and 23-24 stand rejected under 35 U.S.C. §102(e) as being anticipated by Binger '015 (USP 5,661,015). The Examiner asserts that Binger '015 discloses each element of the present invention. Applicants assert that patentable distinction exists between the cited prior art and the present invention.

Distinction Between the Present Invention and Binger '015

Binger '015 discloses DNA sequences coding for Eimeria surface antigens, recombinant vectors containing such DNA sequences, transformed microorganisms containing such vectors, and method for producing the antigens using the transformed microorganisms.

Applicants direct the Examiner to Applicants' response of March 22, 2002 for a discussion on why the 37 kD protein disclosed in Binger '015 is on the surface. Applicants will not repeat this argument here, but still assert the Examiner is erroneous in her assessment of Binger '015.

The Examiner asserts an unjust conclusion: based on the molecular weight and the presence in Eimeria, the Examiner extrapolates the Binger '015 protein to having the same function as the protein of the invention, by stating (on page 7, line 7 of the office action):". . . they appear to possess the same or similar functional characteristics, i.e. LDH activity . . .". This assertion is baseless. More importantly, Applicants can demonstrate that it is untrue. Apart from having an amino acid sequence completely unrelated to the one of the invention, the Binger '015 protein is not an LDH.

For support, Applicants present the following facts. First, Binger '015 fails to disclose the terms Lactate or dehydrogenase anywhere within the patent disclosure. Secondly, Binger '015 fails to disclose a possible function for the protein, let alone

an activity as an enzyme.

Applicants can demonstrate that the Binger '015 protein is not an LDH, by computer analyses that can easily be performed using the program "BlastP" from the NCBI Internet website (URL: http://www.ncbi.nlm.nih.gov/Blast), by applying the function for a conserved domain search. For instance, Applicants have performed the following analyses:

An alignment of the protein from seq. id. no. 2 of the present invention with all entries of the complete NCBI protein database shows significant (*) matches to lactate and malate dehydrogenase enzymes, while such an alignment done with the Binger '015 protein (fig. 32) only results in a few non-significant (*) hits to unrelated proteins.

A computer analysis was performed with the protein from Binger '015 and with the protein of the present invention, for amino acid stretches that represent the characteristic conserved domains shared by all (lactate) dehydrogenase enzymes. Such conserved domains are not present in the Binger '015 protein, while very prominent in the protein of the invention (see enclosures Ap 3, and 10).

(*) significance of an alignment-result from the Blast

programs is represented as "E value"; the smaller this is, the less probability exists that the match found occurred by chance. Rule of thumb: significance starts below 0.1, and becomes stronger the smaller the E value gets, ultimately it can be zero for a full and specific match. Compare for instance the high significance of the matches of the seq. id. 2 protein of the invention: E= 10^{-117} through 10^{-39}, to the non-significant (thus accidental) matches found for the Binger protein: E= 0.3 through 8.9.

Enclosed are printouts of the results of such analyses:

Enclosure-page(s):	Content:
Ap 1 - 7	Results from analyses with Binger protein
1 - 2	BlastP analysis order form
3	Results from conserved domain search
4 - 7	Results from protein database alignment
Ap 8 - 14	Results from analyses with seq. id. 2 protein
8 - 9	BlastP analysis order form
10	Results from conserved domain search
11 - 12	Description of conserved domains detected
13 - 14 (partial)	Results from protein database alignment

"A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." Verdegaal Bros. v. Union Oil Co. of California, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). Binger '015 fails to disclose each and every element as set forth in the instant claims. With the

overwhelming evidence that the Binger '015 protein fails to fall within the scope of the present invention, Applicants respectfully request withdrawal of the 35 U.S.C. §102(e) rejection.

Conclusion

All the stated grounds of the rejections have been properly traversed, accommodated or rendered moot. Applicants respectfully submit that the present application is in condition for allowance.

Attached hereto is a marked-up version to show changes to the application by this amendment.

If the Examiner believes for any reason that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (302) 934-4395, in Millsboro, Delaware.

If necessary, the Commissioner is hereby authorized in this, concurrent, and further replies, to charge payment or credit any overpayment to Deposit Account No. 02-2334 for any additional

fees required under 37 C.F.R. §1.16 or under 37 C.F.R. §1.17; particularly extension of time fees.

Respectfully submitted,

Mark W. Milstead
Patent Counsel
Registration No. 45,825

Attorney Docket NO. I/95150-US/D1

Intervet Inc.
Patent Department
405 State Street
P.O. Box 318
Millsboro, DE 19966
Tel: (302) 933-4034
Fax: (302) 933-4013

MWM

Enclosure: Version with Markings to Show Changes Made
- Abstracts of Wolf and Makler references.
- Alignment result and sequence files of AAW33626 (Binger protein) and seq. id. no. 2.
- Pages Ap 1 - 14, BlastP and Conserved domain search results of both seq. id. 2 and the Binger protein, see description above.

Version with Markings to Show Changes Made

In the Specification:

The following paragraph has been added before the paragraph beginning on page 1 line 1.

--This application is a division of U.S. Application No. 08/676,882, filed July 3, 1996, now U.S. Patent No. 6,100,241.--

1: Am J Trop Med Hyg 1993 Feb;48(2):205-10

Measurement of the lactate dehydrogenase activity of Plasmodium falciparum as an assessment of parasitemia.

Makler MT, Hinrichs DJ.

Clinical Pathology and Research Service, Veterans Administration Medic Center, Portland, Oregon.

This report describes an enzyme assay for the detection of Plasmodium falciparum. The assay is based on the observation that the lactate dehydrogenase (LDH) enzyme of P. falciparum has the ability to rapidly use 3-acetyl pyridine NAD (APAD) as a coenzyme in the reaction leadin to the formation of pyruvate from lactate. Human red blood cell LDH carries out this reaction at a very slow rate in the presence of APAD. We measured the development of APADH and found that the formation of th product could establish the basis of an assay that detected the presence of P. falciparum from in vitro cultures at parasitemia levels of 0.02%. We al had occasion to use this assay with clinical samples. We found a correlation between levels of parasitemia and the activity of parasite LDH Parasite LDH (pLDH) activity could be measured in blood hemolysates and in plasma and serum from patients with malaria. We used the serum assay for pLDH and followed the level of pLDH in a patient with cerebra malaria prior to antimalarial treatment and during the recovery period. From these initial studies, it is evident that the measurement of pLDH has correlation with parasitemia and may offer a method that can be develope into a simple test for the detection of Plasmodium parasitemia.

PMID: 8447524 [PubMed - indexed for MEDLINE]

Reference molecule: AAW33626 1 - 178 (178 aa) Homology

Sequence 2: SEQ_ID_2.TXT 1 - 330 (330 aa) 25%

Alignment type: Global Protein
Parameters: Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N

```
AAW33626     (     1) tsreapgaspp-akrrrtslgapaagegplrrweqpaa---------gtaaai-------
SEQ_ID_2.TXT (     1) mavfekntrpkiamvgsgmiggtmaflcslrelgdvvlfdvvpnmpmgkamdishnssvv

AAW33626     (    44) ----------------------------------------rqqleereqqrqreqqlqhvr
SEQ_ID_2.TXT (    61) dtgitvygsnsyeclkgadvviitagitkipgksdkewsrmdllpvnikimrevgaaiks

AAW33626     (    65) stpgraaavqarlnawvaegnklpese----------------rrrrmleqymnl----
SEQ_ID_2.TXT (   121) ycp--nafvinitnpldvmvaalqessglphhricgmagmldssrfrrmiadklevsprd

AAW33626     (   104) ----------------------------ekvkklrkkldeeaearakyiegefkknphwg
SEQ_ID_2.TXT (   179) vqgmvigvhgdhmvplsryatvngiplsefvkkgwikqeevddivqktkvaggeivrllg

AAW33626     (   136) plkaenpllpfaqreadeayrrf----------------------------grgapsag
SEQ_ID_2.TXT (   239) qgsayyapgasaiqma-esylkdrkrvmvcscylqgqygvqnhylgvpcviggrgvekii

AAW33626     (   167) plrekmlgarr----------------------k
SEQ_ID_2.TXT (   298) el-eltaqerqelqgsidevkemqkaiaaldask
```

AAGENESEQ:AAW33626

ID AAW33626 standard; Protein; 178 AA.

XX

AC AAW33626;

XX

DT 21-MAY-1998 (first entry)

XX

DE Eimeria tenella sporozoite, schizont, merozoite antigen.

XX

KW Coccidiosis; vaccine; poultry; protozoan; parasite; antigen;

KW sporozoite; schizont; merozoite.

XX

OS Eimeria tenella.

XX

FH Key Location/Qualifiers

FT Misc-difference 64

FT /note= "encoded by CAG"

FT Misc-difference 65

FT /note= "encoded by CGC"

XX

PN US5661015-A.

XX

PD 26-AUG-1997.

XX

PF 03-JUN-1988; 88US-0202721.

XX

PR 20-DEC-1991; 91US-0812349.

PR 03-JUN-1988; 88US-0202721.

XX

PA (HOFF) HOFFMANN LA ROCHE INC.

XX

PI Altenburger W, Binger M, Chizzonite RA, Kramer RA;

PI Lomedico PT, McAndrew SJ;

XX

DR WPI; 1997-434379/40.

DR N-PSDB; AAT93598.

XX

PT New DNA from Eimeria tenella and related immunogenic polypeptides -

PT useful in vaccines to protect poultry against coccidiosis

XX

PS Example 6.5; Fig 32; 72pp; English.

XX

CC This 28 kDa protein is recognised by monoclonal antibody 8A2
CC (ATCC HB 9710). This antibody also specifically reacts with an
CC Eimeria tenella 37 kDa surface antigen that is present in the
CC sporozoite, schizont and merozoite developmental stages. The
CC amino acid sequence was deduced from a cDNA clone (see AAT93598)
CC obtained from a cDNA library by immunological screening with
CC monoclonal antibodies raised against Eimeria antigens. The
CC invention provides DNA sequences (see AAT93593-98) coding for Eimeria
CC surface antigens (see AAW31582-84 and AAW33621-26), recombinant vectors
CC containing such DNA sequences, transformed microorganisms
CC containing such vectors, and methods for producing the antigens
CC using the transformed microorganisms. Methods are also provided
CC for protecting poultry against coccidiosis using the Eimeria
CC surface antigens. The surface antigens are administered either as
CC purified proteins or in the form of DNA encoding the proteins in a
CC viral vector such as a vaccinia virus. The vaccines may produce
CC antibodies that are cross-reactive with other Eimeria species.

XX

SQ Sequence 178 AA;

SQ 27 A; 26 R; 5 N; 2 D; 0 B; 0 C; 13 Q; 21 E; 0 Z; 12 G; 2 H;

SQ 2 I; 15 L; 13 K; 3 M; 3 F; 14 P; 6 S; 4 T; 3 W; 3 Y; 4 V;

SQ 0 Others;

tsreapgasp pakrrrtslg apaagegplr rweqpaagta aairqqleer eqqrqreqql
qhvrstpgra aavqarlnaw vaegnklpes errrrmleqy mnlekvkklr kkldeeaear
akyiegefkk nphwgplkae npllpfaqre adeayrrfgr gapsagplre kmlqarrk

//

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Akzo Nobel N.V.
(B) STREET: Velperweg 76
(C) CITY: Arnhem
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 6824 BM
(G) TELEPHONE: 04120-66204
(H) TELEFAX: 04120-50592
(I) TELEX: 37503 akpha nl

(ii) TITLE OF INVENTION: T cell stimulatory protein of Eimeria

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1679 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Eimeria acervulina
(D) DEVELOPMENTAL STAGE: Schizont

(vii) IMMEDIATE SOURCE:
(B) CLONE: EASC2_1

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:280..1269
(D) OTHER INFORMATION:/function= "Eimeria lactate dehydrogenase"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1..51
(D) OTHER INFORMATION:/label= pBluescriptII

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1624..1679
(D) OTHER INFORMATION:/label= pBluescriptII

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:45..54
(D) OTHER INFORMATION:/label= EcoRI-linker

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1621..1630
(D) OTHER INFORMATION:/label= EcoRI-linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTC GGGTTTTTTT      60

TTTTTTTTCT ACACATTAAT ATTCTTCGTT TACGTTTATT TTGCTACAAA TAAACCCCTT     120

AAACTCTCTA TTTCCTCATA TTCTACCGCT TCATCGGTGG GTGTGTAAGA CGTACGTACG     180

TACAGCTGGG GCTGGCTTAC TGCGCACCGC TTATTTATTA CTTAATTCAT ACACATTTTA     240

TATCTTTCTT CTTCTTTTTT CTTGCTCTTT CTTGTGAAA ATG GCG GTC TTC GAG        294
                                              Met Ala Val Phe Glu
                                                1               5

AAG AAT ACA CGC CCC AAG ATT GCT ATG GTG GGC TCC GGT ATG ATT GGA       342
Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly Ser Gly Met Ile Gly
                  10                  15                  20

GGC ACC ATG GCT TTC CTG TGC AGC TTG AGG GAA CTC GGA GAT GTT GTC       390
Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu Leu Gly Asp Val Val
              25                  30                  35

CTC TTC GAC GTT GTA CCG AAC ATG CCG ATG GGG AAG GCG ATG GAT ATA       438
Leu Phe Asp Val Val Pro Asn Met Pro Met Gly Lys Ala Met Asp Ile
          40                  45                  50

TCG CAC AAT TCG TCG GTG GTT GAC ACG GGT ATA ACA GTA TAC GGC TCA       486
Ser His Asn Ser Ser Val Val Asp Thr Gly Ile Thr Val Tyr Gly Ser
      55                  60                  65

AAT TCA TAC GAG TGC TTG AAG GGT GCG GAC GTA GTA ATA ATA ACA GCA       534
Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val Val Ile Ile Thr Ala
  70                  75                  80                  85

GGG ATA ACA AAG ATA CCC GGA AAG AGC GAT AAA GAA TGG TCT AGA ATG       582
Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys Glu Trp Ser Arg Met
                  90                  95                 100

GAT CTA TTA CCT GTG AAT ATA AAG ATA ATG AGG GAG GTC GGT GCA GCA       630
Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg Glu Val Gly Ala Ala
             105                 110                 115

ATT AAA TCT TAC TGT CCT AAT GCA TTT GTT ATT AAT ATA ACA AAT CCT       678
Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile Asn Ile Thr Asn Pro
         120                 125                 130

TTA GAT GTG ATG GTA GCT GCT CTT CAA GAG TCA TCA GGA CTA CCT CAT       726
Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser Ser Gly Leu Pro His
     135                 140                 145

CAT AGA ATC TGC GGT ATG GCT GGG ATG CTT GAT AGC TCT CGT TTT AGA       774
His Arg Ile Cys Gly Met Ala Gly Met Leu Asp Ser Ser Arg Phe Arg
150                 155                 160                 165

CGT ATG ATA GCT GAT AAA TTA GAA GTC TCT CCT AGA GAT GTA CAG GGG       822
Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro Arg Asp Val Gln Gly
                 170                 175                 180

ATG GTC ATA GGT GTA CAC GGC GAT CAT ATG GTG CCC CTA AGT AGA TAT       870
Met Val Ile Gly Val His Gly Asp His Met Val Pro Leu Ser Arg Tyr
             185                 190                 195
```

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GCA ACA GTT AAC GGC ATC CCG CTT TCT GAG TTT GTT AAG AAG GGC TGG        918
Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe Val Lys Lys Gly Trp
        200                 205                 210

ATC AAG CAA GAA GAA GTA GAT GAT ATC GTT CAG AAG ACC AAG GTC GCT        966
Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln Lys Thr Lys Val Ala
    215                 220                 225

GGA GGA GAG ATC GTA CGC CTA TTA GGA CAA GGC TCT GCT TAC TAT GCT       1014
Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly Ser Ala Tyr Tyr Ala
230                 235                 240                 245

CCA GGG GCT TCA GCT ATT CAG ATG GCT GAG AGC TAT CTA AAG GAT AGA       1062
Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser Tyr Leu Lys Asp Arg
                250                 255                 260

AAG AGA GTG ATG GTT TGC TCT TGC TAC TTG CAA GGA CAA TAT GGT GTA       1110
Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln Gly Gln Tyr Gly Val
            265                 270                 275

CAG AAT CAC TAC TTA GGA GTA CCT TGT GTT ATC GGT GGG AGA GGT GTT       1158
Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile Gly Gly Arg Gly Val
        280                 285                 290

GAG AAG ATT ATT GAG TTA GAA TTG ACC GCA CAA GAA AGA CAG GAG CTT       1206
Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln Glu Arg Gln Glu Leu
    295                 300                 305

CAG GGA TCT ATC GAT GAG GTT AAG GAG ATG CAG AAG GCT ATT GCT GCT       1254
Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln Lys Ala Ile Ala Ala
310                 315                 320                 325

CTT GAT GCA TCC AAG TAAGCAGCAG CAAAATCGCA GAAGTTGCAG CGCTAGAACA       1309
Leu Asp Ala Ser Lys
                330

ACCAGCAGCA GCAGCAGCAG CAGCCTATAG TTCTTGCTGC TGCTGTTCCT ACTACAGCTG     1369

CGGCTTTCTT CCTCGTGTTA TTATCATGAT AGTAAGCTGC TGTACCAGCA GCAGCAGCAG     1429

CAGCAGATTT TGCTTGCACC GCCGTTTGTT TTGCGTACAC CGGCAGAAAT ATTGACTTGC     1489

AGTTAGGAGA AAGAAAGAAA ACAAACACGA TCCCATCGAT CCCAATAAAC CCCACACTGT     1549

CGATCCCATC GATCCCAGCA ACTCCACGGG GCTCTTAACT GTTAAACCTA TTATTCTTAT     1609

CATTACTGTC TCCCGAATTC GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC     1669

CCGGTACCCA                                                            1679
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Val Phe Glu Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly
 1               5                  10                  15

Ser Gly Met Ile Gly Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu
            20                  25                  30

Leu Gly Asp Val Val Leu Phe Asp Val Val Pro Asn Met Pro Met Gly
```

```
         35                  40                  45

Lys Ala Met Asp Ile Ser His Asn Ser Ser Val Val Asp Thr Gly Ile
     50                  55                  60

Thr Val Tyr Gly Ser Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val
 65                  70                  75                  80

Val Ile Ile Thr Ala Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys
                 85                  90                  95

Glu Trp Ser Arg Met Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg
            100                 105                 110

Glu Val Gly Ala Ala Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile
        115                 120                 125

Asn Ile Thr Asn Pro Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser
    130                 135                 140

Ser Gly Leu Pro His His Arg Ile Cys Gly Met Ala Gly Met Leu Asp
145                 150                 155                 160

Ser Ser Arg Phe Arg Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro
                165                 170                 175

Arg Asp Val Gln Gly Met Val Ile Gly Val His Gly Asp His Met Val
            180                 185                 190

Pro Leu Ser Arg Tyr Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe
        195                 200                 205

Val Lys Lys Gly Trp Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln
    210                 215                 220

Lys Thr Lys Val Ala Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly
225                 230                 235                 240

Ser Ala Tyr Tyr Ala Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser
                245                 250                 255

Tyr Leu Lys Asp Arg Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln
            260                 265                 270

Gly Gln Tyr Gly Val Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile
        275                 280                 285

Gly Gly Arg Gly Val Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln
    290                 295                 300

Glu Arg Gln Glu Leu Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln
305                 310                 315                 320

Lys Ala Ile Ala Ala Leu Asp Ala Ser Lys
                325                 330
```

NCBI

Nucleotide Protein Translations Retrieve results for an RID

protein–protein **BLAST**

Search
tsreapgasppakrrrtslgapaagegplrrweqpaagtaaairqqleereqqrqreq
ql
qhvrstpgraaavqarlnawvaegnklpeserrrrmleqymnlekvkklrkkldeeae
ar
akyiegefkknphwgplkaenpllpfaqreadeayrrfgrgapsagplrekmlqarrk

Set subsequence From: To:

Choose database nr

Do CD-Search ☑

Now: BLAST! or Reset query Reset all

Options for advanced blasting

Limit by entrez query or select from: (none)

Composition-based statistics ☑

Choose filter ☑ Low complexity ☐ Mask for lookup table only ☐ Mask lower case

Expect 10

Word Size 3

Matrix BLOSUM62 Gap Costs Existence: 11 Extension: 1

PSSM

Other advanced

PHI pattern

Format

Show ☑ Graphical Overview ☑ Linkout ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query or select from: (none)

Expect value range:

Layout: Two Windows Formatting options on page with results: None

Autoformat Semi-auto

BLAST! or Reset all

Get the URL with preset values ? Get URL

NCBI

Nucleotide Protein formatting BLAST Translations Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (178 letters)

No putative conserved domains have been detected

The request ID is 1031904890-06049-27032

Format! or Reset all

The results are estimated to be ready in 9 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query or select from: (none)

Expect value range:

NCBI

results of BLAST

BLASTP 2.2.4 [Aug-26-2002]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1031904190-027664-9746

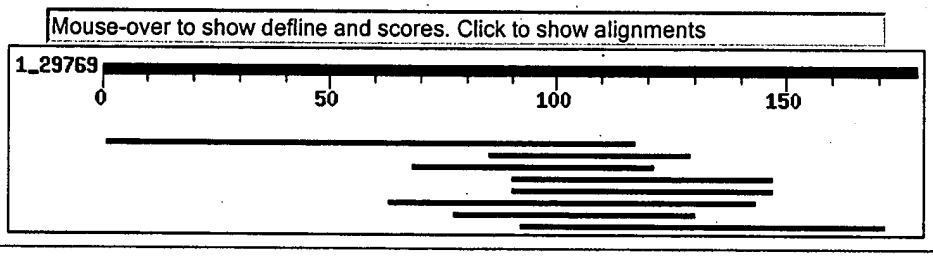
Query=
(178 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,044,513 sequences; 330,426,180 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 8 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value	
gi|3309614|gb|AAC26124.1| (AF073462) serine rich protein [E...	35	0.30	
gi|17508897|ref|NP_492564.1| (NM_060163) T05F1.11.p [Caenor...	35	0.30	L
gi|19115578|ref|NP_594666.1| (NC_003424) putative DNA repai...	34	0.61	
gi|20349350|ref|XP_112453.1| (XM_112453) similar to hypothe...	32	2.9	L
gi|20888303|ref|XP_146514.1| (XM_146514) similar to hypothe...	32	2.9	L
gi|20837540|ref|XP_130281.1| (XM_130281) similar to oxyster...	31	5.3	L
gi|12025422|gb|AAG45917.1|AF309776_1 (AF309776) guanylyl cy...	31	7.8	
gi|6739527|gb|AAF27289.1|AF140613_1 (AF140613) N-hydroxylat...	30	8.9	

Alignments

Get selected sequences | Select all | Deselect all

>gi|3309614|gb|AAC26124.1| (AF073462) serine rich protein [Eimeria acervulina
Length = 271

Score = 35.4 bits (80), Expect = 0.30
Identities = 39/128 (30%), Positives = 57/128 (44%), Gaps = 11/128 (8%)

```
Query: 2   SREAPGASPPAKRRRTS-------LGAPAAGEGPLRRWEQ----PAAGTAAAIXXXXXXX 50
           S   PG S   ++R  S         A  +G  P RR  +    P +G   A
Sbjct: 131 SSPQPGPSAGTRKRPPSDAAARYLAAAEGSGGSPKRRRVETRGMPPSGLVKARSQDAEDR 190

Query: 51  XXXXXXXXXXXHVRSTPGRAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKKLR 110
                  +V  TPG+A  V+  L + V EGNK  E +RR  ML++YM+  +V++ R
Sbjct: 191 DEQTRRQALGLNVTRTPGKADRVRNLLGSKVEEGNKKTERQRREEMLKEYMDHPRVQETR 250

Query: 111 KKLDEEAE 118
            K+D +AE
Sbjct: 251 DKVDRDAE 258
```

>gi|17508897|ref|NP_492564.1| L (NM_060163) T05F1.11.p [Caenorhabditis elegar
gi|7507212|pir||T24545 hypothetical protein T05F1.11 - Caenorhabditis elegans
gi|3924855|emb|CAB04699.1| (Z81586) predicted using Genefinder-contains simila
domain: PF00646 (F-box domain.), Score=37.6,
E-value=9.2e-08, N=1-cDNA EST yk579e12.3 comes from this
gene-cDNA EST yk579e12.5 comes from this gene
[Caenorhabditis elegans]
Length = 1003

Score = 35.4 bits (80), Expect = 0.30
Identities = 18/45 (40%), Positives = 28/45 (62%), Gaps = 1/45 (2%)

```
Query: 86  KLPESERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKYIEGEFKK 130
           KL E E+R+R+LE+ M +++ K    K+  EAE R K  + E K+
Sbjct: 792 KLKEEEKRKRVLEEEMEMKR-KNEEAKIKLEAEMREKAEQAEIKR 835
```

>gi|19115578|ref|NP_594666.1| (NC_003424) putative DNA repair protein [Schizc
gi|7492536|pir||T37672 probable DNA repair protein - fission yeast (Schizosac
pombe)
gi|6138896|emb|CAB59685.1| (AL132675) putative DNA repair protein [Schizosacch
Length = 1375

Score = 34.3 bits (77), Expect = 0.61
Identities = 21/54 (38%), Positives = 30/54 (54%), Gaps = 10/54 (18%)

```
Query: 69  RAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKKLRKKLDEEAEARAK 122
           R AAV   +N +V+      E+E     LE+Y  +E +KK  K LD++AE R K
Sbjct: 842 RVAAVSGTINTFVSH-----ETE-----LEKYKLIESIKKSEKSLDKQAEERDK 885
```

>gi|20349350|ref|XP_112453.1| L (XM_112453) similar to hypothetical protein F
Length = 4600

Score = 32.3 bits (72), Expect = 2.9
Identities = 22/61 (36%), Positives = 31/61 (50%), Gaps = 9/61 (14%)

```
Query: 91   ERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKYIEGEFK---KNPHWGPLKAENPLLPFA 147
           ER++R LE+     + KKL+++L+ + E      E E K   K P  GP   E P L  A
Sbjct: 1927 ERKKRELERLAKEMQEKKLQQELERQKE      EDELKRKVKRDKAGDAAKEEDDLKKA 1980
```

```
Query: 148  Q 148
            Q
Sbjct: 1981 Q 1981
```

>gi|20888303|ref|XP_146514.1| (XM_146514) similar to hypothetical protein I
Length = 3053

```
 Score = 32.0 bits (71), Expect = 2.9
 Identities = 22/61 (36%), Positives = 31/61 (50%), Gaps = 9/61 (14%)

Query: 91  ERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKYIEGEFK---KNPHWGPLKAENPLLPFA 147
           ER++R LE+     + KKL+++L+ + E      E E K   K P  GP   E P L  A
Sbjct: 380 ERKKRELERLAKEMQEKKLQQELERQKE------EDELKRKVKRPKAGPAAKEEPPLKKA 433

Query: 148 Q 148
           Q
Sbjct: 434 Q 434
```

>gi|20837540|ref|XP_130281.1| (XM_130281) similar to oxysterol-binding prot
OSBP-related protein 6 [Mus musculus]
Length = 820

```
 Score = 31.2 bits (69), Expect = 5.3
 Identities = 25/85 (29%), Positives = 41/85 (47%), Gaps = 7/85 (8%)

Query: 64  RSTPGRAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKY 123
           R  P +    +  L A  AE  ++ E +R RR   +  NLE + K  KK+  +A  R  +
Sbjct: 738 RFRPDQRFLEEGNLEAAAAEKQRVEELQRSRRRYMEENNLEHIPKFFKKVI-DANQREAW 796

Query: 124 IEG----EFKKNPHWGPLKAENPLL 144
           +      E +K+P  G  K ++P+L
Sbjct: 797 VSNDTYWELRKDP--GFSKVDSPVL 819
```

>gi|12025422|gb|AAG45917.1|AF309776_1 (AF309776) guanylyl cyclase [Heteroder
Length = 949

```
 Score = 30.8 bits (68), Expect = 7.8
 Identities = 19/64 (29%), Positives = 34/64 (52%), Gaps = 10/64 (15%)

Query: 78  NAWVAEGNKLPESERRRRMLEQY-----MNL-----EKVKKLRKKLDEEAEARAKYIEGE 127
           + WV   ++ P  E+ R+ L Q       +NL     + +++    KL+EE + R K +EGE
Sbjct: 646 DCWVETPSERPTIEKVRQKLRQMGAQRRVNLMDHVFDMLEQYANKLEEEVQERTKELEGE 705

Query: 128 FKKN 131
            +K+
Sbjct: 706 KRKS 709
```

>gi|6739527|gb|AAF27289.1|AF140613_1 (AF140613) N-hydroxylating cytochrome P4
Length = 542

```
 Score = 30.4 bits (67), Expect = 8.9
 Identities = 22/80 (27%), Positives = 36/80 (44%)
```

```
           R+ +  + ++  + K L  K  EEA+    YI  +FK N +     A         R+
Sbjct: 158 RKILTSEIISPARHKWLHDKRAEEADNLVFYIHNQFKANKNVNLRTATRHYGGNVIRKMV 217

Query: 153 EAYRRFGRGAPSAGPLREKM 172
           + R FG+G P  GP  E++
Sbjct: 218 FSKRYFGKGMPDGGPGPEEI 237
```

Get selected sequences | Select all | Deselect all

```
  Database: All non-redundant GenBank CDS
  translations+PDB+SwissProt+PIR+PRF
    Posted date:  Sep 4, 2002 12:20 AM
  Number of letters in database: 330,426,180
  Number of sequences in database:  1,044,513

Lambda     K      H
   0.313    0.130    0.379

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 109,376,468
Number of Sequences: 1044513
Number of extensions: 3934752
Number of successful extensions: 13080
Number of sequences better than 10.0: 53
Number of HSP's better than 10.0 without gapping: 10
Number of HSP's successfully gapped in prelim test: 43
Number of HSP's that attempted gapping in prelim test: 13046
Number of HSP's gapped (non-prelim): 74
length of query: 178
length of database: 330,426,180
effective HSP length: 113
effective length of query: 65
effective length of database: 212,396,211
effective search space: 13805753715
effective search space used: 13805753715
T: 11
A: 40
X1: 16 ( 7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.9 bits)
S2: 67 (30.4 bits)
```

NCBI

Nucleotide Protein Translations protein–protein BLAST Retrieve results for an RID

Search
MAVFEKNTRPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSS
VV
DTGITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAI
KS
YCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRD

Set subsequence From: To:

Choose database nr

Do CD-Search ☑

Now: BLAST! or Reset query Reset all

Options for advanced blasting

Limit by entrez query or select from: (none)

Composition-based statistics ☑

Choose filter ☑ Low complexity ☐ Mask for lookup table only ☐ Mask lower case

Expect 10

Word Size 3

Matrix BLOSUM62 Gap Costs Existence: 11 Extension: 1

PSSM

Other advanced

PHI pattern

Format

Show ☑ Graphical Overview ☑ Linkout ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query or select from: (none)

Expect value range:

Layout: Two Windows Formatting options on page with results: None

Autoformat Semi-auto

BLAST! or Reset all

Get the URL with preset values ? Get URL

NCBI

formatting **BLAST**

Nucleotide | Protein | Translations | Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (330 letters)

Putative conserved domains have been detected, click on the image below for detailed results.

The request ID is 1031904433-0681-18522

Format! or Reset all

The results are estimated to be ready in 7 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query or select from: (none)

Expect value range:

NCBI

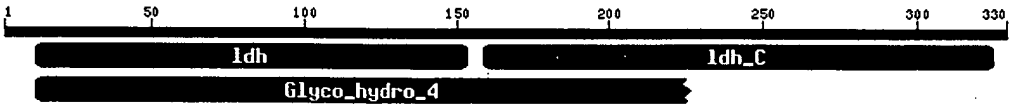
NCBI Conserved Domain Search


```
RPS-BLAST 2.2.3 [Apr-24-2002]

Query= local sequence:
         (330 letters)

Database: oasis_sap.v1.58
           4540 PSSMs; 885,521 total columns
```

Click on boxes for multiple alignments



Show Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download **Cn3D**!

PSSMs producing significant alignments:	Score (bits)	E value
gnl|CDD|4825 pfam02866, ldh_C, lactate/malate dehydrogenase, alpha/beta C-t...	138	2e-34
gnl|CDD|5846 pfam00056, ldh, lactate/malate dehydrogenase, NAD binding doma...	110	8e-26
gnl|CDD|2579 pfam02056, Glyco_hydro_4, Family 4 glycosyl hydrolase	40.6	7e-05

- gnl|CDD|4825, pfam02866, ldh_C, lactate/malate dehydrogenase, alpha/beta C-terminal domain. L-lactate dehydrogenases are metabolic enzymes which catalyse the conversion of L-lactate to pyruvate, the last step in anaerobic glycolysis. L-2-hydroxyisocaproate dehydrogenases are also members of the family. Malate dehydrogenases catalyse the interconversion of malate to oxaloacetate. The enzyme participates in the citric acid cycle. L-lactate dehydrogenase is also found as a lens crystallin in bird and crocodile eyes.

```
CD-Length = 171 residues,  98.8% aligned
Score =  138 bits (350), Expect = 2e-34

Query:  158  MLDSSRFRRMIADKLEVSPRDVQGMVIGVHGDHMVPLSRYATVNGIPLSEFVK-KGWIKQ  216
Sbjct:  2    RLDSARARTLLAEKLGVDPRSVHVYIIGEHGDSEVPVWSHANVTGVPLESLVKELGKDSD  61

Query:  217  EEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYG  276
Sbjct:  62   DELEELIERVQDAGYEVIKA--KGSTTYSIALAGARIAKAILRDTNGVLPVSVYLDGFYG  119

Query:  277  VQNH-YLGVPCVIGGRGVEKIIELELTAQERQELQGSIDEVKEMQKAIAAL  326
Sbjct:  120  IPDDVYFSVPVVLGRNGVEEIVELPLNDFEREKLEKSADELKKIIEKGFAF  170
```

- gnl|CDD|5846, pfam00056, ldh, lactate/malate dehydrogenase, NAD binding domain. L-lactate dehydrogenases are metabolic enzymes which catalyse the conversion of L-lactate to pyruvate,

of the family. Malate dehydrogenases catalyse the interconversion of malate to oxaloacetate. The enzyme participates in the citric acid cycle. L-lactate dehydrogenase is also found as a lens crystallin in bird and crocodile eyes. N-terminus (this family) is a Rossman NAD-binding fold. C-terminus is an unusual alpha+beta fold.

```
            CD-Length = 145 residues,  96.6% aligned
            Score =  110 bits (276), Expect = 8e-26

Query:  11   KIAMVG-SGMIGGTMAFLCSLRELG-DVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYG  68
Sbjct:  5    KVAVVGAGGGVGSSLAFALALQGLADELVLVDINKDKAEGVAMDLQHGAAFLLVPG-IIG  63

Query:  69   SNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI  128
Sbjct:  64   GDDYEALKDADVVVITAGVPRKPGMT-----RLDLLNRNAKIFKDIVPALAKSAPDAIVL  118

Query:  129  NITNPLDVMVAALQESSGLPHHRICG  154
Sbjct:  119  VVSNPVDILTYIAWKVSGFPPERVIG  144
```

---

gnl|CDD|2579, pfam02056, Glyco_hydro_4, Family 4 glycosyl hydrolase.

```
            CD-Length = 416 residues, only  57.0% aligned
            Score = 40.6 bits (95), Expect = 7e-05

Query:  11   KIAMVGSG---MIGGTMAFLCSLREL--GDVVLFDVVPNM--PMGKAMDISHNSSVVDTG  63
Sbjct:  1    KIVIIGGGSTITPKNLLGDLKRTEELPGRELALYDIDEERLDAIQTLCKKLVDEAGPDIK  60

Query:  64   ITVYGSNSYECLKGADVVIITAGITKIPGKSDKE----------------------WSRMD  102
Sbjct:  61   FEKT-TDRKEALKDADFVINAIRVGLLPARELDEKIPLRHGVVGTIQETVGPGGIFRGLR  119

Query:  103  LLPVNIKIMREVGAAIKSYCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSS  162
Sbjct:  120  TIPVFFDIAK----DMEELCPDAWMLNYTNPAAMVTEAVYRRY--PNIKAIGLCHSPIGI  173

Query:  163  RFRRMIADKLEVSPRDVQGMVIGVHGDHMVPLS--RYATVNGIP-LSEFVKKGWIKQEEV  219
Sbjct:  174  KER--LAKALGLDRDDIRVRVAGL--NHMAWLLEVRYNGDDLYPKLREEVAQYGKDGQKE  229

Query:  220  DDIVQKTK  227
Sbjct:  230  KNIQGAPW  237
```

Sequences producing significant alignments:	Score (bits)	E Value
gi|2497625|sp|Q27797|LDH_TOXGO L-lactate dehydrogenase (LDH...	422	e-117
gi|1695772|gb|AAC47443.1| (U35118) lactate dehydrogenase [T...	364	e-100
gi|17986421|ref|NP_539055.1| (NC_003317) MALATE DEHYDROGENA...	337	9e-92
gi|16127885|ref|NP_422449.1| (NC_002696) malate dehydrogena...	327	1e-88
gi|2554656|pdb|1LDG| Plasmodium Falciparum L-Lactate Dehyd...	327	2e-88
gi|2497624|sp|Q27743|LDH1_PLAFD L-lactate dehydrogenase (LD...	326	3e-88
gi|4699811|pdb|1CEQ|A Chain A, Chloroquine Binds In The Cof...	325	6e-88
gi|3183070|sp|O33525|MDH_RHILV MALATE DEHYDROGENASE >gi|262...	320	1e-86
gi|13094954|gb|AAK12097.1| (AF323520) lactate dehydrogenase...	317	1e-85
gi|15966809|ref|NP_387162.1| (NC_003047) PROBABLE MALATE DE...	316	3e-85
gi|15889894|ref|NP_355575.1| (NC_003062) AGR_C_4782p [Agrob...	315	6e-85
gi|17936514|ref|NP_533304.1| (NC_003304) malate dehydrogena...	313	2e-84
gi|15214056|sp|P93052|LDH_BOTBR L-lactate dehydrogenase (LD...	304	9e-82
gi|13473642|ref|NP_105210.1| (NC_002678) malate dehydrogena...	302	4e-81
gi|15892443|ref|NP_360157.1| (NC_003103) malate dehydrogena...	298	7e-80
gi|15604243|ref|NP_220759.1| (NC_000963) MALATE DEHYDROGENA...	293	3e-78
gi|16079964|ref|NP_390790.1| (NC_000964) malate dehydrogena...	280	1e-74
gi|10444017|gb|AAG17668.1|AF274310_1 (AF274310) lactate deh...	275	4e-73
gi|2497856|sp|Q59202|MDH_BACIS MALATE DEHYDROGENASE >gi|743...	275	8e-73
gi|7387870|sp|Q9X4K8|MDH_BACTC MALATE DEHYDROGENASE >gi|473...	270	2e-71
gi|15615720|ref|NP_244024.1| (NC_002570) malate dehydrogena...	266	2e-70
gi|21402635|ref|NP_658620.1| (NC_003995) ldh, lactate/malat...	265	5e-70
gi|13541928|ref|NP_111616.1| (NC_002689) Malate dehydrogena...	255	6e-67
gi|16081997|ref|NP_394412.1| (NC_002578) probable malate de...	244	1e-63
gi|21228068|ref|NP_633990.1| (NC_003901) Malate dehydrogena...	243	2e-63
gi|2506848|sp|P80040|MDH_CHLAU MALATE DEHYDROGENASE >gi|201...	241	6e-63
gi|22405888|gb|ZP_00000751.1| (NZ_AAAA01000052) hypothetica...	241	1e-62
gi|21674327|ref|NP_662392.1| (NC_002932) malate dehydrogena...	237	2e-61
gi|20149959|pdb|1GV0|A Chain A, Structural Basis For Thermo...	236	4e-61
gi|20149955|pdb|1GUZ|A Chain A, Structural Basis For Thermo...	230	2e-59
gi|3183534|sp|P80038|MDH_CHLVI MALATE DEHYDROGENASE >gi|176...	229	5e-59
gi|20149961|pdb|1GV1|A Chain A, Structural Basis For Thermo...	228	1e-58
gi|16331672|ref|NP_442400.1| (NC_000911) 2-ketoacid dehydro...	225	7e-58
gi|20089703|ref|NP_615778.1| (NC_003552) malate dehydrogena...	223	3e-57
gi|15606841|ref|NP_214221.1| (NC_000918) malate dehydrogena...	220	2e-56
gi|17231814|ref|NP_488362.1| (NC_003272) malate dehydrogena...	219	4e-56
gi|15606767|ref|NP_214147.1| (NC_000918) malate dehydrogena...	211	1e-53
gi|14600880|ref|NP_147405.1| (NC_000854) malate dehydrogena...	209	3e-53
gi|18313295|ref|NP_559962.1| (NC_003364) malate dehydrogena...	197	1e-49
gi|15672358|ref|NP_266532.1| (NC_002662) L-lactate dehydrog...	180	2e-44
gi|80325|pir||A25805 L-lactate dehydrogenase (EC 1.1.1.27) ...	177	1e-43
gi|16799319|ref|NP_469587.1| (NC_003212) similar to L-lacta...	176	3e-43
gi|2506808|sp|P13714|LDH_BACSU L-lactate dehydrogenase (L-LDH)	176	3e-43
gi|16077374|ref|NP_388187.1| (NC_000964) L-lactate dehydrog...	176	4e-43
gi|16802256|ref|NP_463741.1| (NC_003210) similar to L-lacta...	176	5e-43
gi|126059|sp|P00345|LDH_BACME L-lactate dehydrogenase (L-LD...	174	1e-42
gi|126053|sp|P14561|LDHP_BACPS L-lactate dehydrogenase P (L...	171	1e-41
gi|21397481|ref|NP_653466.1| (NC_003995) ldh, lactate/malat...	171	1e-41
gi|21402918|ref|NP_658903.1| (NC_003995) ldh_C, lactate/mal...	170	2e-41
gi|15893559|ref|NP_346908.1| (NC_003030) L-lactate dehydrog...	169	5e-41
gi|126054|sp|P20619|LDHX_BACPS L-lactate dehydrogenase X (L...	167	2e-40
gi|21399802|ref|NP_655787.1| (NC_003995) ldh, lactate/malat...	166	3e-40
gi|17367583|sp|Q59244|LDH_BACCL L-lactate dehydrogenase (L-...	166	5e-40
gi|230128|pdb|1LLC| L-Lactate Dehydrogenase (E.C.1.1.1.27)...	165	7e-40
gi|80070|pir||S00019 L-lactate dehydrogenase (EC 1.1.1.27) ...	164	1e-39
gi|11251151|pir||T44580 lactate dehydrogenase [imported] - ...	163	2e-39
gi|1730106|sp|P50934|LDH_LACSK L-lactate dehydrogenase (L-L...	163	3e-39

US 093908460GP1

Creation date: 12-15-2003
Indexing Officer: TLO - TRUC P LO
Team: OIPEBackFileIndexing
Dossier: 09390846

Legal Date: 05-15-2003

No.	Doccode	Number of pages
1	SRNT	45
2	NPL	6
3	NPL	10
4	NPL	15
5	NPL	16
6	NPL	16
7	NPL	15
8	NPL	9
9	NPL	6
10	NPL	7
11	NPL	3
12	NPL	2

Total number of pages: 150

Remarks:

Order of re-scan issued on .....